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RA MEDLINE: 99124785; PubMed: 9927117;
R1 Kelleher, J., Pearson, W.N., Harwood, S.H., Funk, C.J., Evans, J.L.,
RA Slattery, T.M., Rehm, M.G.,
R1 "Sequence and analysis of the genome of a baculovirus pathogenetic for
R1 Limnoria dispar."
R1 Virology 253:17-34(1999).
R1
R1 SEQUENCE FROM N.A.
R1 Kelleher, J.
R1 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
R1 EMBL: AF081810; AAC70345.1;
R1
R1 SEQUENCE 53 AA; 5513 MW; A32BB7D15263DD00 CRC64;
SQ

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Query Match 39.5%; Score 58.5; DR 12; Length 54;
 Best Local Similarity 44.8%; Pred. No. 0.052;
 Matches 14; Conservative 3; Mismatches 8; Indels 5; Gaps 2;

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UY 2 C1XSGDLCFRSDHICCGSGKCAFCV--CL 27
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Gb 25 CACGTGACVCHSDE--CGSGKCGSPFNVCY 51

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RESULT 7
 ID 090658 PRELIMINARY: PRI: 78 AA.
 AC 090658;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE CONOTOXIN SCAPOLD VI/VII.
 OS Conus pennaceus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conus.
 CX NCBI_TaxID=37335;
 RX SEQUENCE FROM N.A.
 RP MEDLINE: 21105649; PubMed: 11158371;
 RA Kelleher, J.S.G., Gilad Y., Avilan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 R1 "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."
 R1 Mol. Biol. Evol. 18:120-131(2001).
 R1 EMBL: AF193255; AAP07667.1;
 R1 InterPro: IP004214; Conotoxin.
 R1 Pfam: PF02950; Conotoxin_1.
 R1 SEQUENCE 78 AA; 8615 MW; 90411ACBB7FE3FB CRC64;
 SQ

Query Match 36.8%; Score 56; DR 5; Length 78;
 Best Local Similarity 80.0%; Pred. No. 0.18;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 17 CCGSGKCAFCV 26
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Gb 64 CCGSGKCAFCV 73

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RESULT 8
 ID 090656 PRELIMINARY: PRI: 78 AA.
 AC 090656;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE CONOTOXIN SCAPOLD VI/VII.
 OS Conus textile (Cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conus.
 CX NCBI_TaxID=3436;
 RX SEQUENCE FROM N.A.
 RP MEDLINE: 21105649; PubMed: 11158371;
 RA Kelleher, J.S.G., Gilad Y., Avilan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 R1 "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."
 R1 Mol. Biol. Evol. 18:120-131(2001).
 R1 EMBL: AF193255; AAP07667.1;
 R1 InterPro: IP004214; Conotoxin.
 R1 Pfam: PF02950; Conotoxin_1.
 R1 SEQUENCE 78 AA; 8615 MW; 90411ACBB7FE3FB CRC64;
 SQ

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RA Fainzilber M.;
R1 "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."  

R1 Mol. Biol. Evol. 18:120-131(2001).  

R1 EMBL: AF193255; AAP07667.1;  

R1 InterPro: IP004214; Conotoxin.  

R1 Pfam: PF02950; Conotoxin_1.  

R1 SEQUENCE 78 AA; 8756 MW; D1004F903066415E CRC64;  

SQ

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Query Match 36.8%; Score 56; DR 5; Length 78;
 Best Local Similarity 42.2%; Pred. No. 0.18;
 Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 2;

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UY 53 CCGSGDLCFRSDHICCGSGKCAFCV 77
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Gb 53 CCGSGDLCFRSDHICCGSGKCAFCV 77

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RESULT 9
 ID 090660 PRELIMINARY: PRI: 80 AA.
 AC 090660;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE CONOTOXIN SCAPOLD VI/VII.
 OS Conus pennaceus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conus.
 CX NCBI_TaxID=37335;
 RX SEQUENCE FROM N.A.
 RP MEDLINE: 21105649; PubMed: 11158371;
 RA Kelleher, J.S.G., Gilad Y., Avilan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 R1 "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."
 R1 Mol. Biol. Evol. 18:120-131(2001).
 R1 EMBL: AF193255; AAP07667.1;
 R1 InterPro: IP004214; Conotoxin.
 R1 Pfam: PF02950; Conotoxin_1.
 R1 SEQUENCE 80 AA; 9194 MW; C1DC2A6F9F388C944 CRC64;
 SQ

Query Match 35.7%; Score 55; DR 5; Length 80;
 Best Local Similarity 37.7%; Pred. No. 0.22;
 Matches 11; Conservative 3; Mismatches 9; Indels 7; Gaps 2;

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QY 2 C1XSGDLCFRSDHICCGSGKCAFCV 27
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Gb 52 C1XSGDLCFRSDHICCGSGKCAFCV 76

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RESULT 10
 ID 090A73 PRELIMINARY: PRI: 67 AA.
 AC 090A73;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE CONOTOXIN SCAPOLD VI/VII.
 OS Conus abbreviatus.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conus.
 CX NCBI_TaxID=16125;
 RX SEQUENCE FROM N.A.
 RP MEDLINE: 95339555; PubMed: 16354766;
 RA Duda T.P., Orr, J., Columbia S.R.;
 RA "Molecular genetics of ecological diversification: duplication and
 R1 rapid evolution of toxin genes of the venomous gastropod Conus."
 R1 Proc. Natl. Acad. Sci. U.S.A. 96:1623-1627(1999).
 R1 EMBL: AF030671; AAD48224.1;
 SQ

Best Local Similarity 42.98; Pred. No. 0.46;
Matches 9; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 2 MASBLERFSDH100 SEQR 22
1 1 1 1 1 1 1
14 10 MVDSPELGNH-IPNSDRC 65

RESULT 15

Q4110

PRELIMINARY; PRI: 153 AA.

AC Q4110;

D1 01-087-2001 (TEMBLER, 19, created)

D1 01-087-2001 (TEMBLER, 19, last sequence update)

D1 01-087-2001 (TEMBLER, 19, last annotation update)

DE P04812.38 PROTEIN.

GN P04812.38.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Liliopsida;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eriobotryaceae; Oryzaceae; Oryza.

XX NCBI_taxid:4530;

RN 111

RP SEQUENCE FROM N.A.

RC SIKAIN-CV, NIPPONHARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 1, PAC

clone-p04812.38";

PI Submitted (JAN 2001) to the EMBL/GenBank/DBJ databases.

LV EMBL: AF003076; BAB56053.1;

SV SEQUENCE 153 AA; 16959 MW; 2E64874FA7BFAE10 CRC64;

Query Match 35.28; Score 53.5; LB 10; Length 153;

Best Local Similarity 52.48; Pred. No. 0.83;

Matches 11; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 12 SDHICGSGKQAF---VCL 27

111 11 11 11

14 104 SDHIVGCLGKGVFLNNIVCV 124

Search completed: September 19, 2002, 09:26:45
Job time: 417 sec



Search results using SW model

Sequence: 1 X01XSGH/CFRSHH/HGCSKCAVCL 27

Search: 105224 seqs, 18719550 residues

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post-processing: Minimum Match 0.8

Database: 1 SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary: 105224

Sequence: 1 X01XSGH/CFRSHH/HGCSKCAVCL 27

Search: 105224 seqs, 18719550 residues

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post-processing: Minimum Match 0.8

Database: 1 SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary: 105224

Sequence: 1 X01XSGH/CFRSHH/HGCSKCAVCL 27

Search: 105224 seqs, 18719550 residues

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post-processing: Minimum Match 0.8

Database: 1 SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary: 105224

Sequence: 1 X01XSGH/CFRSHH/HGCSKCAVCL 27

Search: 105224 seqs, 18719550 residues

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post-processing: Minimum Match 0.8

Database: 1 SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary: 105224

Sequence: 1 X01XSGH/CFRSHH/HGCSKCAVCL 27

Search: 105224 seqs, 18719550 residues

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post-processing: Minimum Match 0.8

Prod. No.	Score	Match	Length	Database	Accession
1	42.8	76	1	OX02_CONTE	OX02_CONTE
2	42.5	76	1	OX02_CONTE	OX02_CONTE
3	42.5	76	1	OX02_CONTE	OX02_CONTE
4	42.5	76	1	OX02_CONTE	OX02_CONTE
5	42.5	76	1	OX02_CONTE	OX02_CONTE
6	42.5	76	1	OX02_CONTE	OX02_CONTE
7	42.5	76	1	OX02_CONTE	OX02_CONTE
8	42.5	76	1	OX02_CONTE	OX02_CONTE
9	42.5	76	1	OX02_CONTE	OX02_CONTE
10	42.5	76	1	OX02_CONTE	OX02_CONTE
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12	42.5	76	1	OX02_CONTE	OX02_CONTE
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14	42.5	76	1	OX02_CONTE	OX02_CONTE
15	42.5	76	1	OX02_CONTE	OX02_CONTE
16	42.5	76	1	OX02_CONTE	OX02_CONTE
17	42.5	76	1	OX02_CONTE	OX02_CONTE
18	42.5	76	1	OX02_CONTE	OX02_CONTE
19	42.5	76	1	OX02_CONTE	OX02_CONTE
20	42.5	76	1	OX02_CONTE	OX02_CONTE
21	42.5	76	1	OX02_CONTE	OX02_CONTE
22	42.5	76	1	OX02_CONTE	OX02_CONTE
23	42.5	76	1	OX02_CONTE	OX02_CONTE
24	42.5	76	1	OX02_CONTE	OX02_CONTE
25	42.5	76	1	OX02_CONTE	OX02_CONTE
26	42.5	76	1	OX02_CONTE	OX02_CONTE
27	42.5	76	1	OX02_CONTE	OX02_CONTE
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31	42.5	76	1	OX02_CONTE	OX02_CONTE
32	42.5	76	1	OX02_CONTE	OX02_CONTE
33	42.5	76	1	OX02_CONTE	OX02_CONTE
34	42.5	76	1	OX02_CONTE	OX02_CONTE
35	42.5	76	1	OX02_CONTE	OX02_CONTE
36	42.5	76	1	OX02_CONTE	OX02_CONTE
37	42.5	76	1	OX02_CONTE	OX02_CONTE
38	42.5	76	1	OX02_CONTE	OX02_CONTE
39	42.5	76	1	OX02_CONTE	OX02_CONTE
40	42.5	76	1	OX02_CONTE	OX02_CONTE
41	42.5	76	1	OX02_CONTE	OX02_CONTE
42	42.5	76	1	OX02_CONTE	OX02_CONTE
43	42.5	76	1	OX02_CONTE	OX02_CONTE
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45	42.5	76	1	OX02_CONTE	OX02_CONTE

ALIGNMENTS

RESULT 1

OX02_CONTE 1

16-oct-2001 (bel. 40, Last sequence update)

16-oct-2001 (bel. 40, Last annotation update)

Omega-type conotoxin (X02 precursor)

OX02

Bukaryolus (Cloth-of-gold cone)

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010 EMBL: 0797007 AAC59137.1
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012 KW Signal:
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014 FT SIGNAL 1 16 PROTEIN-LIKE
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software version 4.5
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EM protein protein search using sw model

Run on: September 19, 2002 09:21:16 Search time: 51.99 seconds

(without alignments)
57,584 Million cell updates/sec

Title: US-09-749-637a-271

Refined score: 152

Sequence: 1 XGKSCDELFESMIGGSCGAFVNL 27

Scoring matrix:

BLOSUM62
Gapop 19.0, Export 0.5

Searched: 747574 seqs, 11074796 residues

Total number of hits satisfying chosen parameters: 247074

Minimum hit seq length: 7

Maximum hit seq length: 2000000000

Post-processing: Minimum Match: 5%

Listing hits: 40 Summaries

Hit database:

AA005970: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 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2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2

[illegible]

Matches	Conservative	Mismatches	Indels	Gaps
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08	11	11	0	0
09	2	2	0	0
10	2	2	0	0
11	1	1	0	0
12	1	1	0	0
13	1	1	0	0
14	1	1	0	0
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96	1	1	0	0
97	1	1	0	0
98	1	1	0	0
99	1	1	0	0
100	1	1	0	0

CC neuropathic pain, nociceptive pain, the disorder is inflammation or a
 CC cardiorespiratory failure. A cardiac rhythm of the heart is
 CC alleviate pain in a mammal in pain or about to be subjected to a pain
 CC existing event, and to treat disorders associated with radical
 CC depolarization of excitable membranes by a treatment of a pain
 CC disorders include cardiac, vascular and cerebral ischemia and asthma.
 XX

Sequence: 41 AA:

Query Match: 84.6% Score: 127, 1b: 22, Length: 41
 Best Local Similarity: 84.6% Prod. No.: 9, 4e-08
 Matches: 22, Conservative: 0, Mismatches: 4, Indels: 0, Gaps: 0

2: C(XS)DQKRSKSHQVTSKAVPTL 27
 11: 111111111111111111111111
 1b: 6: C(S)SDDHPSDHSKAKAKVPTL 41

FIGURE 1

AMINOACID

1b: AMINOACID standard: peptide: 41 AA:

XX AMINOACID:

11: 24-oct-2001 (first entry)

1b: 24-oct-2001 (first entry)

1b: 24-oct-2001 (first entry)

1b: 24-oct-2001 (first entry)

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 11: 111111111111111111111111
 1b: 6: C(S)SDDHPSDHSKAKAKVPTL 41

FIGURE 1

AMINOACID

1b: AMINOACID standard: peptide: 41 AA:

XX AMINOACID:

11: 24-oct-2001 (first entry)

1b: 24-oct-2001 (first entry)

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1b: 24-oct-2001 (first entry)

1b: 24-oct-2001 (first entry)

1b: 24-oct-2001 (first entry)

Database version 4.5
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M protein: protein search, using SW model

Run on: September 19, 2002, 09:15:44 : Search time 21.85 seconds
(without alignment)
30,183 Matches with update/2002

Hit: US-09-749-637a-271

Percent score: 15%

Sequence: 1 KXHSKLLTRESIRGSSSEAVVTL 27

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 23128 seqs, 2412594 residues

Total number of hits satisfying chosen parameters: 23128

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Displaying first 45 summaries

Database: Issued Patients_AA*

1 US-09-749-637a-271
2 US-09-749-637a-271
3 US-09-749-637a-271
4 US-09-749-637a-271
5 US-09-749-637a-271

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match Length	Score	Database
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3	51.5	49.1	46	2	US-08-682-485A-4
4	50.5	49.1	46	2	US-08-682-485A-4
5	50.5	49.1	46	2	US-08-682-485A-4
6	50.5	49.1	46	2	US-08-682-485A-4
7	50.5	49.1	46	2	US-08-682-485A-4
8	50.5	49.1	46	2	US-08-682-485A-4
9	50.5	49.1	46	2	US-08-682-485A-4
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13	50.5	49.1	46	2	US-08-682-485A-4
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15	50.5	49.1	46	2	US-08-682-485A-4
16	50.5	49.1	46	2	US-08-682-485A-4
17	50.5	49.1	46	2	US-08-682-485A-4
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22	50.5	49.1	46	2	US-08-682-485A-4
23	50.5	49.1	46	2	US-08-682-485A-4
24	50.5	49.1	46	2	US-08-682-485A-4
25	50.5	49.1	46	2	US-08-682-485A-4
26	50.5	49.1	46	2	US-08-682-485A-4
27	50.5	49.1	46	2	US-08-682-485A-4

28	49.5	49.5	47	1	US-08-117-080-3
29	49.5	49.5	47	1	US-08-471-329-1
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37	49.5	49.5	47	2	US-08-915-142-1
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RESULTS

RESULT 1

Sequence 4: Application US-08-92485A

Patent No. 5761668

GENERAL INFORMATION:

APPLICANT: AIRSIR, K. S. K. R.

APPLICANT: AIRSIR, K. S. K. R.

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APPLICANT: AIRSIR, K. S. K. R.

APPLICANT: AIRSIR, K. S. K. R.

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APPLICANT: AIRSIR, K. S. K. R.

APPLICANT: AIRSIR, K. S. K. R.

UNPUBLISHED: No
 ANTI-SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Atrax robustus
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 37
 OTHER INFORMATION: /label-4
 OTHER INFORMATION: /label-4
 OTHER INFORMATION: of biological activity
 US-08-087-489A-4

Query Match: 40.1%; Score 61; DB 1; Length 47;
 Post Local Similarity: 47.8%; Prod. Re. 0.8%;
 Matches: 11; Conservative: 4; Mismatches: 7; Indels: 2; Gaps: 1;

2 2 1XSDUP-PROBIOGEN-SUBVAF-24
 1 1 1 1 1 1 1 1 1
 4 1XSDUP-PROBIOGEN-SUBVAF-24

RESULT 2

US-08-087-489A-4

Sequence 4; Application US/089444

Patent No. 5950182

GENERAL INFORMATION:

APPLICANT: ALKERMES, INC.

APPLICANT: HODDER, MICHAEL E.

APPLICANT: TYLER, MARGARET J.

APPLICANT: WENAR, EDWARD J.

TITLE OF INVENTION: Insecticidal Toxins derived from

NUMBER OF INVENTION: 10001 Web Address: http://www.alkermes.com

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Zeneva, Inc.

STREET: 1200 South 47th Street

CITY: Richmond

STATE: California

COUNTRY: USA

ZIP: 94804

COMPUTER RELEVABLE DATA:

MEDIUM TYPE: Floppy disk

COMPILE: IBM PC compatible

SOFTWARE: Patented Release #1.0, Version #1.25

CLASSIFICATION: 4.24

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

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APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

UNPUBLISHED: No
 ANTI-SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Atrax robustus
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 37
 OTHER INFORMATION: /label-4
 OTHER INFORMATION: /label-4
 OTHER INFORMATION: of biological activity
 US-08-087-489A-4

Query Match: 40.1%; Score 61; DB 1; Length 47;
 Post Local Similarity: 47.8%; Prod. Re. 0.8%;
 Matches: 11; Conservative: 4; Mismatches: 7; Indels: 2; Gaps: 1;

2 2 1XSDUP-PROBIOGEN-SUBVAF-24
 1 1 1 1 1 1 1 1 1
 4 1XSDUP-PROBIOGEN-SUBVAF-24

RESULT 3

US-08-087-489A-4

Sequence 6; Application US/089444

Patent No. 5955573

GENERAL INFORMATION:

APPLICANT: ALKERMES, INC.

APPLICANT: HODDER, MICHAEL E.

APPLICANT: TYLER, MARGARET J.

APPLICANT: WENAR, EDWARD J.

TITLE OF INVENTION: Insecticidal Toxins derived from

NUMBER OF INVENTION: 10001 Web Address: http://www.alkermes.com

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Zeneva, Inc.

STREET: 1200 South 47th Street

CITY: Richmond

STATE: California

COUNTRY: USA

ZIP: 94804

COMPUTER RELEVABLE DATA:

MEDIUM TYPE: Diskette

COMPILE: IBM compatible

SOFTWARE: Patented Release #1.0, Version #1.25

CLASSIFICATION: 4.24

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

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FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

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APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

APPLICATION NUMBER: US/089444

FILING DATE: 29 JAN 1994

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1 RESULT 8
 2 DS-07 689 6946-6
 3 Sequence 6, Application No. 97070696-646
 4 Patent No. 524011
 5
 6 GENERAL INFORMATION:
 7
 8 APPLICANT: Baldovino M. Alford
 9
 10 TITLE OF INVENTION: Separated foldout portions
 11
 12 TITLE OF INVENTION: For Small Discrete-Block Papers
 13
 14 NUMBER OF SEQUENCES: 25
 15
 16 CORRESPONDENCE ADDRESS:
 17
 18 ADDRESSEE: ThePro, No. 524011th & Western
 19
 20 STREET: 9045 South 700 East, Suite 200
 21
 22 CITY: Sandy
 23
 24 STATE: Utah
 25
 26 COUNTRY: USA
 27
 28 ZIP: 84070

COMPILED RETABLE FROM:
MEDIUM TYPE: Diskette, A-5 inch, 720 kb storage
COMPUTER: COMPAQ LITE/86
OPERATING SYSTEM: DOS 4.01
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
ACQUISITION NUMBER: B9507048, 6948
FILING DATE: 1991qdr
CLASSIFICATION: 540
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0000
FILING DATE: 00
ALTERNATIVE INFORMATION:
NAME: WALTER H. MATHIAS
REGISTRATION NUMBER: 200,000
REFERENCE/CITATION NUMBER: 0000
REFERENCES/INFORMATION:
TELEPHONE: (601) 566-6644
TELEFAX: (601) 566-0750
REF ID: A9507048
COUNTRY OF ORIGIN: USA
LENGTH: 27 microfiches
TYPE: AMIN-ACTD
POPULATION: 11000
MICROFILM TYPE: microfiche
REMARKS:
NAME: FREDERICK S. GORDON JR.
CURRENT CITATION NUMBER: 0000
FILING DATE: 1991qdr, 6948

US-07-689-0948-6

Q6173 Matrix	4.70%	Protein	50%	File 1:	Location 2.7:
Best Local Similarity	42.0%	Prot. No.	100		
Matches 1:	Conserved	2:	Mismatches	11:	Indels
					2: gaps
QY	2	STX14L-PROTEIN	2580	ATTA	46
	1	1	1	1	1
	1	1	1	1	1
1b	2	STX14L-PROTEIN	2580	ATTA	46

1 PERSONAL INFORMATION:
 2 AFFILIANT: ALEXANDER, R. E. GORDON
 3 AFFILIANT: B. WELCH, MARGARET E.
 4 AFFILIANT: TYLER, MARGARET E.
 5 AFFILIANT: V. NARR, EDWARD J.
 6 TITLE OF INVENTION: Dissociated loci for isolated from
 7 TITLE OF INVENTION: Dissociated loci for isolated from
 8 NUMBER OF INVENTORS: 26
 9 ADDRESS: 1260 South 47th Street
 10 CITY: Richmond
 11 STATE: California
 12 COUNTRY: USA
 13 ZIP: 94804
 14
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC DOS/MS DOS
 19 SOFTWARE: Patent Release #1.0, Version #1.25
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/942,185A
 22 FILING DATE:
 23 CLASSIFICATION: 424
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: US/08/942,185
 26 FILING DATE: 17 JULY 1996
 27 AFFILIANT NUMBER: US/08/942,185, 933
 28 FILING DATE: 27 JULY 1994
 29 APPLICATION NUMBER: WO 94/15108
 30 FILING DATE: 29 JAN 1994
 31 APPLICATION NUMBER: AU 110722
 32 FILING DATE: 31 JAN 1992
 33 ATTORNEY/AGENT INFORMATION:
 34 NAME: Shaw, Melissa A.
 35 REGISTRATION NUMBER: 36,401
 36 REFERENCE/DOCKET NUMBER: 110 5079/201
 37 TELECOMMUNICATION INFORMATION:
 38 TELEPHONE: 510-231-1142
 39 TELEFAX: 510-231-1112
 40 INFORMATION FOR SEQ. ID NOS.:
 41 SEQUENCE CHARACTERISTICS:
 42 LENGTH: 47 amino acids
 43 TYPE: amino acid
 44 TOPOLOGY: linear
 45 MOLECULE TYPE: protein
 46 HYPOTHEICAL: No
 47 ANTI-SENSE: No
 48 ORIGINAL SOURCE:
 49 ORGANISM: Ataxia formidabilis
 50 FEATURE:
 51 NAME/KEY: Method site
 52 LOCATION: 47
 53 OTHER INFORMATION: /Label 4
 54 OTHER INFORMATION: 70000 "this site may be mutated without loss
 55 OTHER INFORMATION: of biological activity"
 56 US-08-942-185A-B

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 2 Best Local Similarity 43.53% Prod. No. 14
 3 Matches 10 Conserved 3 Mismatches 8 Indels 2 Gaps 1
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1 RESULT: 10
 2 US-08-942-114-B
 3 Sequence 8, Application US/08/942-114
 4 Patent No. 5950182

1 PERSONAL INFORMATION:
 2 AFFILIANT: ALEXANDER, R. E. GORDON
 3 AFFILIANT: B. WELCH, MARGARET E.
 4 AFFILIANT: TYLER, MARGARET E.
 5 AFFILIANT: V. NARR, EDWARD J.
 6 TITLE OF INVENTION: Dissociated loci for isolated from
 7 TITLE OF INVENTION: Dissociated loci for isolated from
 8 NUMBER OF INVENTORS: 26
 9 ADDRESS: 1260 South 47th Street
 10 CITY: Richmond
 11 STATE: California
 12 COUNTRY: USA
 13 ZIP: 94804
 14
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC DOS/MS DOS
 19 SOFTWARE: Patent Release #1.0, Version #1.25
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/942,185A
 22 FILING DATE:
 23 CLASSIFICATION: 424
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: US/08/942,185
 26 FILING DATE: 17 JULY 1996
 27 AFFILIANT NUMBER: US/08/942,185, 933
 28 FILING DATE: 27 JULY 1994
 29 APPLICATION NUMBER: WO 94/15108
 30 FILING DATE: 29 JAN 1994
 31 APPLICATION NUMBER: AU 110722
 32 FILING DATE: 31 JAN 1992
 33 ATTORNEY/AGENT INFORMATION:
 34 NAME: Shaw, Melissa A.
 35 REGISTRATION NUMBER: 36,401
 36 REFERENCE/DOCKET NUMBER: 110 5079/201
 37 TELECOMMUNICATION INFORMATION:
 38 TELEPHONE: 510-231-1542
 39 TELEFAX: 510-231-1112
 40 INFORMATION FOR SEQ. ID NOS.:
 41 SEQUENCE CHARACTERISTICS:
 42 LENGTH: 47 amino acids
 43 TYPE: amino acid
 44 TOPOLOGY: linear
 45 MOLECULE TYPE: protein
 46 HYPOTHEICAL: No
 47 ANTI-SENSE: No
 48 ORIGINAL SOURCE:
 49 ORGANISM: Ataxia formidabilis
 50 FEATURE:
 51 NAME/KEY: Method site
 52 LOCATION: 47
 53 OTHER INFORMATION: /Label 4
 54 OTHER INFORMATION: 70000 "this site may be mutated without loss
 55 OTHER INFORMATION: of biological activity"
 56 US-08-942-114-B

1 Query Match 32.94% Score 5.2 DB 2: Length 47
 2 Best Local Similarity 43.54% Prod. No. 14
 3 Matches 10 Conserved 3 Mismatches 8 Indels 2 Gaps 1
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1 NAME: Holmschuetz, Elza D.
 2 POSITION NUMBER: 33,712
 3 REFERENCE/PROJECT NUMBER: HTA0027X/001
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: (402) 886-1599
 6 INFORMATION FOR SEQ. ID NO.: 2:
 7 SEQUENCE CHARACTERISTICS:
 8 LENGTH: 78 amino acids
 9 TYPE: amino acid
 10 MOLECULE TYPE: linear
 11 US-09-749-637-2

Query Match 42.98: Score 50: 108 2: Length 78:
 Best Local Similarity 42.98: Prod. No. 24:
 Mismatch 11: Conservation 27: Mismatches 11: Indels 2:
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78

RESULT 14
 US-09-749-637-16
 1 Sequence 16: Application US/08716-008
 2 Patent No. 5885569
 3 GENERAL INFORMATION:
 4 APPLICANT: Windass, John D.
 5 TITLE OF INVENTION: Biological Insect Control Agent
 6 NUMBER OF SEQUENCES: 18
 7 CORRESPONDENCE ADDRESS:
 8 ADDRESSEE: ZENBIA INC.
 9 STREET: 1860 Concord Pike
 10 CITY: Wilmington
 11 STATE: DE
 12 COUNTRY: USA
 13 ZIP: 19810
 14 COMPUTER RELEVABLE FORM:
 15 MEDIUM TYPE: floppy disk
 16 COMPUTER: IBM pc compatible
 17 OPERATING SYSTEM: pc-dos/MS DOS
 18 SOFTWARE: Patent Release #1.0, Version #1.25
 19 CURRENT APPLICATION DATA:
 20 APPLICATION NUMBER: 05/2716, 36
 21 FILING DATE: 24-SEP-1996
 22 CLASSIFICATION: 424
 23 PRIOR APPLICATION DATA:
 24 APPLICATION NUMBER: 05/2716/09677
 25 FILING DATE: 27-MAR-1995
 26 PRIOR APPLICATION DATA:
 27 APPLICATION NUMBER: 08-9405561.5
 28 FILING DATE: 25-MAR-1994
 29 ATTORNEY/AGENT INFORMATION:
 30 NAME: Holmschuetz, Elza D.
 31 REGISTRATION NUMBER: 42,712
 32 REFERENCE/PROJECT NUMBER: HTA0027X/001
 33 TELECOMMUNICATION INFORMATION:
 34 TELEPHONE: (402) 886-1599
 35 INFORMATION FOR SEQ. ID NO.: 16:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 78 amino acids
 38 TYPE: amino acid
 39 MOLECULE TYPE: linear
 40 US-09-749-637-16

Query Match 42.98: Score 50: 108 2: Length 78:
 Best Local Similarity 42.98: Prod. No. 24:
 Mismatch 11: Conservation 27: Mismatches 11: Indels 2:

27 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78

RESULT 15
 PCT US96-05262-14
 1 Sequence 14: Application 16:7/US96-05262
 2 GENERAL INFORMATION:
 3 APPLICANT: Shen, Ki-Joon
 4 APPLICANT: Gilley, Michelle M.
 5 APPLICANT: Gilley, Baldomero M.
 6 APPLICANT: Wash, Kent, Poju
 7 APPLICANT: Marsh, Marc
 8 APPLICANT: Cruz, Lourdes J.
 9 APPLICANT: Alliyard, David R.
 10 TITLE OF INVENTION: Conotoxin Peptides
 11 NUMBER OF SEQUENCES: 14
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Ventria, Inc.
 14 STREET: 1201 New York Avenue, N.W., Suite 1000
 15 CITY: Washington
 16 STATE: DC
 17 COUNTRY: U.S.A.
 18 ZIP: 20005
 19 COMPUTER RELEVABLE FORM:
 20 MEDIUM TYPE: floppy disk
 21 COMPUTER: IBM pc compatible
 22 OPERATING SYSTEM: pc-dos/MS DOS
 23 SOFTWARE: Patent Release #1.0, Version #1.30
 24 CURRENT APPLICATION DATA:
 25 APPLICATION NUMBER: 05/2716/05262
 26 FILING DATE: 17-APR-1996
 27 CLASSIFICATION:
 28 PRIOR APPLICATION DATA:
 29 APPLICATION NUMBER: 05-08/424,561
 30 FILING DATE: 17-APR-1995
 31 ATTORNEY/AGENT INFORMATION:
 32 NAME: SARG, Stephen A.
 33 REGISTRATION NUMBER: 38,609
 34 REFERENCE/PROJECT NUMBER: 21260-107674
 35 TELECOMMUNICATION INFORMATION:
 36 TELEPHONE: 202-962-4848
 37 TELEFAX: 202-962-8800
 38 INFORMATION FOR SEQ. ID NO.: 14:
 39 SEQUENCE CHARACTERISTICS:
 40 LENGTH: 78 amino acids
 41 TYPE: amino acid
 42 STRANDEDNESS: single
 43 TOPOLOGY: linear
 44 MOLECULE TYPE: protein
 45 HYDROLYTIC: NO
 46 PCT-US96-05262-14

Query Match 42.98: Score 50: 108 2: Length 78:
 Best Local Similarity 42.98: Prod. No. 24:
 Mismatch 11: Conservation 27: Mismatches 11: Indels 2:

Search completed: September 19, 2002, 09:14:44
 Job # Time of run



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• M protein - protein search, using sw model

Run on: September 19, 2002, 09:19:14 ; Search time: 51.99 seconds

(without adjustments)
61.357 million cell updates/sec

155 (1974) 6, 27A-27B

Supplement 1

$$Z^{\text{eff}} = Z - \sigma_{\text{eff}} = Z - 1 + \frac{1}{2} \frac{Z}{Z-1} \ln \frac{Z+1}{Z-1} \quad (2)$$
[illegible][illegible]

THE UNIVERSITY OF CHICAGO

Maximum of Seq Length: 0

Post-Processing: Minimum Match 08

May 1990	May 1991	May 1992
1st and 2nd	1st and 2nd	1st and 2nd
3rd and 4th	3rd and 4th	3rd and 4th
5th and 6th	5th and 6th	5th and 6th
7th and 8th	7th and 8th	7th and 8th
9th and 10th	9th and 10th	9th and 10th
11th and 12th	11th and 12th	11th and 12th
13th and 14th	13th and 14th	13th and 14th
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27th and 28th	27th and 28th	27th and 28th
29th and 30th	29th and 30th	29th and 30th
31st	31st	31st

[illegible]

Figure 1 displays a sequence of 16 small images arranged in a 4x4 grid, illustrating the stages of a bird's nest construction. The images show the progression from a single twig to a completed nest with eggs.

[illegible][illegible]

100

[illegible][illegible][illegible]

	Pre-Test	Post-Test
Q1	0.8	0.9
Q2	0.7	0.8
Q3	0.6	0.7
Q4	0.5	0.6
Q5	0.4	0.5
Q6	0.3	0.4
Q7	0.2	0.3
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Q23	0.0	0.0
Q24	0.0	0.0
Q25	0.0	0.0
Q26	0.0	0.0
Q27	0.0	0.0
Q28	0.0	0.0
Q29	0.0	0.0
Q30	0.0	0.0
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Q65	0.0	0.0
Q66	0.0	0.0
Q67	0.0	0.0
Q68	0.0	0.0
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Q94	0.0	0.0
Q95	0.0	0.0
Q96	0.0	0.0
Q97	0.0	0.0
Q98	0.0	0.0
Q99	0.0	0.0
Q100	0.0	0.0

[illegible]

is not greater than or equal to

1000

$$N_{\text{eff}} = 3.36 \pm 0.17 \text{ (stat)} \pm 0.14 \text{ (syst)} \pm 0.11 \text{ (th)} \quad (11)$$

177 1000 21 22 A

[illegible]

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95	22	70	2.0	13.3	1
96	22	70	2.0	13.3	1
97	22	70	2.0	13.3	1
98	22	70	2.0	13.3	1
99	22	70	2.0	13.3	1
100	22	70	2.0	13.3	1

[illegible]

Figure 1 displays a 4x4 grid of 16 small diagrams. Each diagram contains a different geometric shape or pattern, such as a circle, a square, a triangle, or a line, arranged in a grid.

[illegible]



IDENTIFICATION: No
 ANTI SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Atax robustus
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 47
 OTHER INFORMATION: /label 4
 OTHER INFORMATION: /note "this site may be amplified without loss
 of biological activity"
 US 09 749 637a 4

Query Match: 49.5% Score: 799 106 13 Length: 477
 Best Local Similarity: 52.2% Prod. No. 0.0547
 Matches: 123 Conserved: 43 Mismatches: 62 Indels: 27 Gaps: 13

QY 4 CIPSDGCRSDHGGGSGKAF 26
 1111 1 111 111 1
 ID 4 CIPSDGCRSDHGGGSGKAF 24

RESULT 2

US-09-749-637a 4
 Sequence 4: Application US/09933814
 Patent No. 5959182

GENERAL INFORMATION:
 APPLICANT: ALKERM, N. B. SELL, K.
 APPLICANT: HERGEN, JEROME R. H.
 APPLICANT: TYLER, MARCAREL I.
 ALTERNATE: VANDER, ERIC W. J.
 TITLE OF INVENTION: Sequenced folding polymers
 TITLE OF INVENTION: Folded with (Atax of Haplophragma sp. sp.)
 NUMBER OF SEQUENCES: 26
 ADDRESS: Zymo, Inc.
 ADDRESS: Zymo, Inc.
 STREET: 1200 South 17th Street
 CITY: Richmond
 STATE: California
 COUNTRY: USA
 ZIP: 94804
 COMPUTER BEAMABLE FORM:
 METHOD TYPE: Electrophoresis
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Patent in Release #1.0, Version #1.2
 CURRENT APPLICATION DATA:
 FILING DATE: 07/07/99
 CLASSIFICATION: 424
 PREVIOUS APPLICATION DATA:
 NAME: WOSTORFF, M. WAYNE
 REGISTRATION NUMBER: 22,796
 FILING DATE: 27 JULY 1994
 APPLICATION NUMBER: W9/011306
 FILING DATE: 29 JAN 1993
 APPLICATION NUMBER: AT 100722
 FILING DATE: 31 JAN 1992
 AUTHORITY/AGENT INFORMATION:
 NAME: Shaw, Melissa A.
 REGISTRATION NUMBER: 99,001
 REFERENCE/AGENT NUMBER: 99-00000
 IDENTIFICATION INFORMATION:
 TELEPHONE: 510 241 1542
 TELEFAX: 510 241 1112
 IDENTIFICATION NUMBER: 41
 SEQUENCE CHARACTERISTICS:
 LENGTH: 47 amino acids
 TYPE: amino acid
 FEATURE: linear
 M FEATURE TYPE: protein
 IDENTIFICATION: No

ANTI SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Atax robustus
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 47
 OTHER INFORMATION: /label 4
 OTHER INFORMATION: /note "this site may be amplified without loss
 of biological activity"
 US 09 749 637a 4

Query Match: 49.5% Score: 799 106 13 Length: 477
 Best Local Similarity: 52.2% Prod. No. 0.0547
 Matches: 123 Conserved: 43 Mismatches: 62 Indels: 27 Gaps: 13

QY 4 CIPSDGCRSDHGGGSGKAF 26
 1111 1 111 111 1
 ID 4 CIPSDGCRSDHGGGSGKAF 24

RESULT 4

US-07-689-748-5
 Sequence 5: Application US/07090000
 Patent No. 5241011

GENERAL INFORMATION:
 APPLICANT: David Hilliard
 TITLE OF INVENTION: Sequenced folding polymers
 TITLE OF INVENTION: Folded with (Atax of Haplophragma sp. sp.)
 NUMBER OF SEQUENCES: 26
 ADDRESS: Zymo, Inc.
 ADDRESS: Zymo, Inc.
 STREET: 1200 South 17th Street, Suite 200
 CITY: Sandy
 STATE: Utah
 COUNTRY: USA
 ZIP: 84070
 COMPUTER BEAMABLE FORM:
 METHOD TYPE: Electrophoresis
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 FILING DATE: 07/07/99
 CLASSIFICATION: 533
 PREVIOUS APPLICATION DATA:
 NAME: WOSTORFF, M. WAYNE
 REGISTRATION NUMBER: 22,796
 FILING DATE: 27 JULY 1994
 APPLICATION NUMBER: W9/011306
 FILING DATE: 29 JAN 1993
 APPLICATION NUMBER: AT 100722
 FILING DATE: 31 JAN 1992
 AUTHORITY/AGENT INFORMATION:
 NAME: Shaw, Melissa A.
 REGISTRATION NUMBER: 99,001
 REFERENCE/AGENT NUMBER: 99-00000
 IDENTIFICATION INFORMATION:
 TELEPHONE: (801) 566-0643
 TELEFAX: (801) 566-0750
 IDENTIFICATION NUMBER: 41
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: AMINO ACID
 FEATURE: linear
 M FEATURE TYPE: protein
 IDENTIFICATION: No

US-07-689-748-5

Query Match 37.8% Score 66 DB 1 Length 78
 Best Local Similarity 46.4% Prod. No. 0.29
 Matches 13 Conservative 21 Mismatches 11 Indels 2

Query 11 11111111111111111111
 16 51 PWKOSHEMMLAG-NOTREYVW 77

RESULT 4

US-09-749-637a-270-13
 Sequence 13 Application US-09-749-637a-270-13
 Patent No. 5780276

GENERAL INFORMATION:

APPLICANT: SHAG, K1-Japan
 APPLICANT: GILLIG, Michael M.
 APPLICANT: GILLIG, Michael M.
 TITLE OF INVENTION: New method for the
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venetio, David J., Howard & Associates
 STREET: 1201 New York Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: US
 ZIP: 20005

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patgen in Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-749-637a-270-13
 FILING DATE: 07-01-1994

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-09-749-637a-270-13
 FILING DATE: 07-01-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-09-749-637a-270-13
 FILING DATE: 07-01-1994

FILING DATE:

DATE: 07-01-1994

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DATE: 07-01-1994

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DATE: 07-01-1994

FILING DATE:

DATE: 07-01-1994

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DATE: 07-01-1994

FILING DATE:

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FILING DATE:

DATE: 07-01-1994

FILING DATE:

DATE: 07-01-1994

FILING DATE:

DATE: 07-01-1994

FILING DATE:

DATE: 07-01-1994

FILING DATE:

GENERAL INFORMATION:
 APPLICANT: Windass, John D.
 TITLE OF INVENTION: Biological Insect Control Agent
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENICA Inc.
 STREET: 1800 Concord Pike
 CITY: Wilmington
 STATE: DE
 COUNTRY: USA
 ZIP: 19850

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patgen in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-749-637a-270-13
 FILING DATE: 07-01-1994
 CLASSIFICATION: 424

FILING DATE:

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DATE: 07-01-1994

Thu Sep 19 09:49:39 2002

us-09-749-637a-270.ra1

Page 8

Search completed: September 19, 2002, 09:26:44
 Job time: 415 sec

RESEARCH

1111

[illegible]

111	MAY 2000 (TEMPERATURE)
111	MAY 2000 (TEMPERATURE)
111	MAY 2000 (TEMPERATURE)

DOI: 10.1002/1097-4644(200109)19:1<101::AID-JEPM101>3.0.CO;2-1

John's Lividus.

of Negastropoda; Conoidae; Conidae; Conus.

№ 3 - 13810-89426;
[1]
[1]
[1]

ST. JOHN'S, N. Y.

MILLINE 9928955; PubMed 10459796;
Judo T. P. Dambel S. P.

"Molecular genetics of ecological di-

KL. Proc. Natl. Acad. Sci. U.S.A. 96:6822

```
lik EMML: AFD89911; AFD48166.1; -
lik EMML: IPR04214; context:
lik EMML: IPR04214; context:
```

[illegible]

71 AA; 7960 MW; 5153742

Order: Males	42.5%	100%
Host local similarity	44.0%	Pred. N

Methods 11; Conservative 4; Mistm

THE PSYCHOLOGICAL STATE OF THE 28

[illegible]

KISULI 15
Q9JAA6

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11)  Q'0JAA6  PRELIMINARY;  PRI;
AC'  C'0JAA6;

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01-MAY-2000 (TFMHLrel), 13, (Created)

Year	Item	Value
2000	MEMBER: 13, Last	13
2001	MEMBER: 19, Last	19

FOUR-100P CNGOTOXIN LVIR (FRAGMENT)
CNGOTOXIN LVIR.

FILKAR'YATA; M+AZOQ; MOL'USKA; DASTROB
NADASTROBID; CONOLIDAE; CALIDAE; CO-

NOX _1XID-8942b;

THE UNIVERSITY OF CHICAGO

RI: 5.14 min.; 2;
 MH: 1.1 min.; 349.24, 455.57; 1045.97, 66;
 KX

KA Iyoda I. F., J., Palumbi S. R.,
 KT "Molecular genetics of ecological di-

Rapid evolution of toxin genes of the *El Tor* and *Asian* serotypes of *V. cholerae*

PMI; A1089944; AAI048189.1;

146 1470; 14804214; 1490100XII.
149 1490; 14902950; 1490300XII; 1.

SI	STATION	71 AA	79, 14 MW	51(10)9AA
FI	NON_TK	1	1	

Querry Match 32.5%; Score 5

Matches 11; Conservative 4; Mismatch 11; Similarity 44.9%; Pctd. 11

4. **ПРЕДЛОЖЕНИЕ ПОСЛЕДОВАТЕЛЬНОСТИ** 28

```

10: 43 0'5P5GHWCTR--HSPGCTG---PLC 62
      | | : : | | : : | : |

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100

Thu Sep 19 09:49:41 2002

us-09-749-637a-270.rspt

Page 6

GeneBank version 4.5
Copyright (c) 1993-2000 Campbell et al.

EM protein - protein search using sw model

September 19, 2002, 09:29:22 : Search time 11.19 seconds
(without alignment)
85,130 Million cell of data/sec

Hit list
Percent score: 177
Sequence: 1 LRWCFPSHDFPSHDFGYSKQAFVCL 29

Sorting table:
Hit: 8062
Gap: 10.0 : Gap: 0.5
Score: 105224 score: 4879550 residues

Local number of hits satisfying chosen parameters: 105224

Minimum hit seq length: 0
Maximum hit seq length: 20000000

Post-processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

Database: 1 SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

SUMMARIES

Result	Query	Match	Length	DB	Accession
1	66	47.3	27	1	QXDA_GONTE
2	66	47.3	26	1	QXDA_GONTE
3	65	46.7	26	1	QXDA_GONTE
4	64	36.2	27	1	QXDA_GONTE
5	60	33.9	26	1	QXDA_GONTE
6	60	33.9	24	1	QXDA_GONTE
7	58.5	33.1	53	1	QXDA_GONTE
8	58	32.8	47	1	QXDA_GONTE
9	58	32.8	47	1	QXDA_GONTE
10	57.5	31.9	40	1	QXDA_GONTE
11	56.5	31.9	81	1	QXDA_GONTE
12	56.5	31.9	81	1	QXDA_GONTE
13	56	31.6	41	1	QXDA_GONTE
14	56	31.6	41	1	QXDA_GONTE
15	55	31.1	47	1	QXDA_GONTE
16	55	31.1	47	1	QXDA_GONTE
17	55	31.1	47	1	QXDA_GONTE
18	55	31.1	47	1	QXDA_GONTE
19	54.5	30.8	51	1	QXDA_GONTE
20	54	30.5	71	1	QXDA_GONTE
21	54	30.5	71	1	QXDA_GONTE
22	54	30.5	76	1	QXDA_GONTE
23	54	30.5	76	1	QXDA_GONTE
24	53	29.9	71	1	QXDA_GONTE
25	52	29.4	76	1	QXDA_GONTE
26	51	29.1	40	1	QXDA_GONTE
27	51	29.1	40	1	QXDA_GONTE
28	50	28.2	80	1	QXDA_GONTE
29	50	28.2	80	1	QXDA_GONTE
30	49.5	28.3	34	1	QXDA_GONTE
31	49.5	28.3	34	1	QXDA_GONTE
32	49	27.7	24	1	QXDA_GONTE
33	49	27.7	24	1	QXDA_GONTE

ALIGNMENTS

Result	Query	Match	Length	DB	Accession
1	66	47.3	27	1	QXDA_GONTE
2	66	47.3	26	1	QXDA_GONTE
3	65	46.7	26	1	QXDA_GONTE
4	64	36.2	27	1	QXDA_GONTE
5	60	33.9	26	1	QXDA_GONTE
6	60	33.9	24	1	QXDA_GONTE
7	58.5	33.1	53	1	QXDA_GONTE
8	58	32.8	47	1	QXDA_GONTE
9	58	32.8	47	1	QXDA_GONTE
10	57.5	31.9	40	1	QXDA_GONTE
11	56.5	31.9	81	1	QXDA_GONTE
12	56.5	31.9	81	1	QXDA_GONTE
13	56	31.6	41	1	QXDA_GONTE
14	56	31.6	41	1	QXDA_GONTE
15	55	31.1	47	1	QXDA_GONTE
16	55	31.1	47	1	QXDA_GONTE
17	55	31.1	47	1	QXDA_GONTE
18	55	31.1	47	1	QXDA_GONTE
19	54.5	30.8	51	1	QXDA_GONTE
20	54	30.5	71	1	QXDA_GONTE
21	54	30.5	71	1	QXDA_GONTE
22	54	30.5	76	1	QXDA_GONTE
23	54	30.5	76	1	QXDA_GONTE
24	53	29.9	71	1	QXDA_GONTE
25	52	29.4	76	1	QXDA_GONTE
26	51	29.1	40	1	QXDA_GONTE
27	51	29.1	40	1	QXDA_GONTE
28	50	28.2	80	1	QXDA_GONTE
29	50	28.2	80	1	QXDA_GONTE
30	49.5	28.3	34	1	QXDA_GONTE
31	49.5	28.3	34	1	QXDA_GONTE
32	49	27.7	24	1	QXDA_GONTE
33	49	27.7	24	1	QXDA_GONTE

[illegible][illegible]

00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
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00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
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00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79																				

	RESULT	4
TXOF	NAIVE	
TE	TAX_MOVE	STRADDLE
AG	PH1599	
D1	15-JUN-1999 (Rel. 50, Tested)	
D7	15-JUN-1999 (Rel. 50, Last software update)	
L1	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	omega architecture built (50000 Accesses)	
OS	hydroxythe versatula (blue mountains tunnel web spider) (Atax versatus)	
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae; Mesonetales; Pholcidae; Hexathelidae; Hydrogynae;	
OX	MERL_taxID=6964;	
KN	111	
KE	SEQUENCE	
KC	TISSUE:Venom;	
KX	MEHLING_9642154; PubMed 1404195;	
KA	Wong X. E. E. Smith and Fletcher J. A. Wilson B. Wood C. J. J.	
KA	Martin E. H. R. Kim et al.;	
KI	"Structure-function studies of a antiproteolytic peptide and agonist of tissue zellapoptosis of rat aortic endothelial cells"	
KL	Environ. Biochem. 26(4):489-494(1999)	

[illegible]

PI VARIANT 195 195 M V
 SI SEQUENCE 197 AA: 21218 MW: 199068489674579 CR064

Query Match 31.6% Score 56; DI 1; Length 197;
 Host Local Similarity 44.0% Pred. No. 1.9;
 Mismatches 11; Conservative 4; Mismatches 19; Indels 2; Gaps 1;

Q 4 CIPSSMCTPSTOHGVSSECAEV 28
 I 1 1 1 1 1 1 1 1
 I 2 1 KSIQELTF--DHAGETKRPV 101

RESULT 10
 TX BLASTVE STANDARD; PRT: 37 AA.

15-JUL-1999 (rel. 48, Cited)

15-JUL-1999 (rel. 48, last sequence update)

01-MAR-2002 (rel. 41, last annotation update)

FE omega-aristolochin Herb (Acaia Act. Herb);

OS Hadronyche versata (Blue mountains funnel web spider) (Arax

OS veratilis);

OS Hekaryoga Metazoa: Arthropoda: Chelicerata: Arachnida: Araneae;

OS Metatomerphae: Hexathe-lidae: Hadronychae;

KN NCBI TaxID:6504;

KN SPIDRENE;

KN TISSUE-Venom;

KA MEDLINE:99421654; PubMed:10491095;

KA Wain X.-H., Smith R., Fletcher J.L., Wilson H., Wood C.J.,

KA Mollin R.H., King G.F.;

KA "Structure-function studies of omega-aristolochin, a potent antagonist

KA of insect voltage-gated calcium channels.";

KA Eur. J. Biochem. 264:488-494(1999)

CO 1- FUNCTION: INHIBITS INSECT, BUT NOT MAMMALIAN, VOLTAGE-GATED

CO CALCIUM CHANNEL CURRENTS.

CO 1- SUBCELLULAR LOCATION: Secreted.

CO 1- TISSUE SPECIFICITY: Produced by the venomous gland.

CO 1- HEST: J56207; IAXH.

CO calcium channel inhibitor; toxin; Neurotoxin.

FI 1- SILENT 4 38 BY SIMILARITY.

FI 1- SILENT 11 22 BY SIMILARITY.

FI 1- SILENT 17 46 BY SIMILARITY.

FI 1- SILENT 37 AA: 4061 MW: A115058959014E2F CR064;

CO 1- Match 31.6% Score 56; DI 1; Length 197;

CO 1- Host Local Similarity 44.0% Pred. No. 1.9;

CO 1- Mismatches 11; Conservative 4; Mismatches 19; Indels 2; Gaps 1;

Q 4 CIPSSMCTPSTOHGVSSECAEV 26

I 1 1 1 1 1 1 1 1

I 2 4 CIPSSMCTPSTOHGVSSECAEV 24

I 3 4 CIPSSMCTPSTOHGVSSECAEV 24

I 4 4 CIPSSMCTPSTOHGVSSECAEV 24

I 5 4 CIPSSMCTPSTOHGVSSECAEV 24

I 6 4 CIPSSMCTPSTOHGVSSECAEV 24

I 7 4 CIPSSMCTPSTOHGVSSECAEV 24

I 8 4 CIPSSMCTPSTOHGVSSECAEV 24

I 9 4 CIPSSMCTPSTOHGVSSECAEV 24

I 10 4 CIPSSMCTPSTOHGVSSECAEV 24

Search completed: September 19, 2002, 09:27:03

Job time: 400 sec



CV 4 PW15SHLPFESHLH338XK 24
 11 111 111 111
 14 KAAWAVSRWRSSE192VAPR 12

RESULT 7
 1-471

Probable antibiotic polypeptide chlo tridescent virus

C/Spectrum: Chlo tridescent virus

Citation: 24-Mar-1999 #sequence-Revision 24 Mar 1999 #feat_change 20 Aug 1999

C/Accession: F04371

RefSeq: D11100a; C A; Parali, G.

Virus Genes 15: 235-245, 1997

Active: The DNA sequence of chlo tridescent virus between the genome coordinates 6192

C/Accession: F04371

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